

Amendments to the specification

Please amend the specification as shown below.

Please amend the paragraph on page 9, lines 11 through 13 as follows:

Figure 2 depicts the N-terminal leucine repeat structure of the AS3 polypeptide. Numbers above the AS3 sequence indicate the positions as shown in the amino acid sequence of SEQ ID NO. 1 of the blocks where uninterrupted leucine (or isoleucine, valine) heptades occur: positions 55 to 117 of SEQ ID No. 1 (top line); positions 196 to 217 of SEQ ID No. 1 (second line left); positions 241 to 277 of SEQ ID No. 1 (second line right); positions 319 to 355 of SEQ ID No. 1 (bottom line left); and positions 375 to 404 of SEQ ID No. 1 (bottom line right).

Please amend the paragraph on page 9, lines 14 through 23 as follows:

Figure 3 depicts sequence comparisons of the putative Mg-nucleotide triphosphate binding subdomains of AS3 with corresponding subdomains of various protein kinases. The boxes represent the Hanks' conserved subdomains, as indicated above each box. The top lines within the boxes show the consensus β -strand, loop, and α -helical secondary structure elements. The numbers in the second lines indicate the positions as shown in the amino acid sequence of SEQ ID NO. 1 of the corresponding conformations in the AS3 sequence. The actual AS3 motifs are shown in the third line: positions 419 to 424 of SEQ ID NO. 1 (Subdomain I β -strand 1); positions 426 to 433 of SEQ ID NO. 1 (Subdomain I Mg-ATP binding loop); positions 453 to 459 of SEQ ID NO. 1 (Subdomain I β -strand 2); positions 472 to 482 of SEQ ID NO. 1 (Subdomain II β -strand 3); positions 489 to 498 of SEQ ID NO. 1 (Subdomain III α -helix C); positions 509 to 516 of SEQ ID NO. 1 (Subdomain IV β -strand 4); positions 525 to 531 of SEQ ID NO. 1 (Subdomain V β -strand 5); positions 540 to 548 of SEQ ID NO. 1 (Subdomain V α -helix D); and positions 554 to 566 of SEQ ID NO. 1 (Subdomain VIa α -helix E). Hanks' conserved subdomains from protein kinases of close similarity are represented in the lines below each subdomain of the AS3 sequence as indicated in the Figure: for Subdomain I β -strand 1, see

SEQ ID Nos: 7-11; for Subdomain I β -strand 2, see SEQ ID Nos: 12-15; for Subdomain II β -strand 3, see SEQ ID Nos: 19-22; for Subdomain III α -helix C, see SEQ ID Nos: 23-25; for Subdomain IV β -strand 4, see SEQ ID Nos: 27-29; for Subdomain V β -strand 5, see SEQ ID Nos: 30-31; for Subdomain V α -helix D, see SEQ ID Nos.: 33-35; and for Subdomain VIa α -helix E, see SEQ ID Nos: 36-39. The names of the kinases are indicated in parentheses. Identical residues are highlighted. In the Mg-ATP binding loop, the “x” and lower case letters indicate non-conserved amino acids.

Please amend the paragraph on page 10, lines 3 through 8 as follows:

Figure 5 depicts the genomic and cDNA positions as shown in SEQ ID NO. 1 of exons in the AS3 transcript. Asterisks represent the exon-intron boundaries. The area between asterisks represents the exons. Exon sequences are in upper case, the numbers represent cDNA positions as shown in the nucleotide sequence of SEQ ID NO. 1. Lower case letters are intron sequences, with the nucleotide sequences shown in Figure 5 for the 3' end of each intron adjacent to the respective 5' end of each exon is found as follows: for the intron junction at Exon 2, see SEQ ID No.: 40; for the intron junction at Exon 3, see SEQ ID No.: 41; for the intron junction at Exon 4, see SEQ ID No.: 42; for the intron junction at Exon 5, see SEQ ID No.: 43; for the intron junction at Exon 6, see SEQ ID No.: 44; for the intron junction at Exon 7, see SEQ ID No.: 45; for the intron junction at Exon 8, see SEQ ID No.: 46; for the intron junction at Exon 9, see SEQ ID No.: 47; for the intron junction at Exon 10, see SEQ ID No.: 48; for the intron junction at Exon 11, see SEQ ID No.: 49; for the intron junction at Exon 12, see SEQ ID No.: 50; for the intron junction at Exon 13, see SEQ ID No.: 51; for the intron junction at Exon 14, see SEQ ID No.: 52; for the intron junction at Exon 15, see SEQ ID No.: 53; for the intron junction at Exon 16, see SEQ ID No.: 54; for the intron junction at Exon 17, see SEQ ID No.: 55; for the intron junction at Exon 18, see SEQ ID No.: 56; for the intron junction at Exon 19, see SEQ ID No.: 57; for the intron junction at Exon 20, see SEQ ID No.: 58; for the intron junction at Exon 21, see SEQ ID No.: 59; for the intron junction at Exon 22, see SEQ ID No.: 60; for the intron junction at Exon 23, see SEQ ID No.: 61; for the intron junction at Exon 24, see SEQ ID No.: 62; for the intron junction at Exon 25, see SEQ ID No.: 63; for the intron junction at Exon 26, see SEQ ID No.: 64; for the intron junction at Exon 27, see SEQ ID No.: 65; for the intron junction at Exon

28, see SEQ ID No.: 66; for the intron junction at Exon 29, see SEQ ID No.: 67; for the intron junction at Exon 30, see SEQ ID No.: 68; for the intron junction at Exon 31, see SEQ ID No.: 69; for the intron junction at Exon 32, see SEQ ID No.: 70; for the intron junction at Exon 33, see SEQ ID No.: 71; and for the intron junction at Exon 34, see SEQ ID No.: 72. Numbers of the first exon indicate positions in PAC26H23. Numbers in parenthesis refer to positions on cosmid 267p19, while numbers in brackets refer to PAC49J10 positions.

Please amend the paragraph on page 10, lines 9 through 18 as follows:

Figure 6. depicts the cDNA sequence and predicted amino acid sequence of human AS3 having an additional 84 base pairs of untranslated 5' sequence as compared to the sequence presented in Fig. 1. The nucleotide sequence corresponds to 1 to 5337 of SEQ ID NO: 4. The amino acid sequence shown corresponds to amino acids 1 to 1391 of SEQ ID NO: 2. The coding region without the 5' and 3' untranslated regions of the human AS3 gene is shown in SEQ ID NO: 3. Numbers on the left indicate positions in base pairs. The amino acid sequence of the open reading frame is depicted under the coding strand. Numbers on the right indicate amino acid positions. Destabilizing signals found in the untranslated regions of AS3 are underlined and the polyadenylation signal and cleavage signal are at base pair positions 5312-5317 and 5333-5337, respectively. The number 5337 found in parentheses at the 3' terminus of the nucleotide sequence in Figure 6-2 indicates the position of the nucleotide residue T located to the left of the 18 residue polyA sequence.